

Copy sent with notice to applicant

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/526,073
Source: IFWP
Date Processed by STIC: 7/6/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/526,073

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ✓ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/526,073

DATE: 07/06/2006
 TIME: 13:47:49

Input Set : A:\PTO.SS.txt
 Output Set: N:\CRF4\07062006\J526073.raw

3 <110> APPLICANT: TAKARA BIO INC.
 5 <120> TITLE OF INVENTION: Thermostable RNase H
 7 <130> FILE REFERENCE: 663952
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/526,073
 C--> 9 <141> CURRENT FILING DATE: 2005-02-28
 9 <150> PRIOR APPLICATION NUMBER: JP 2002-254153
 10 <151> PRIOR FILING DATE: 2002-08-30
 12 <160> NUMBER OF SEQ ID NOS: 16

*see item 4 on Euro
 summary
 sheet*

ERRORRED SEQUENCES

14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 211
 16 <212> TYPE: PRT
 17 <213> ORGANISM: Archaeoglobus profundus
 E--> 19 <400> SEQUENCE: *916 change to*
 20 Met Ile Ala Gly Ile Asp Glu Ala Gly Lys Gly Pro Val Ile Gly
 21 1 5 10 15
 22 Pro Leu Val Ile Cys Gly Val Leu Cys Asp Glu Glu Thr Val Glu
 23 20 25 30
 24 Tyr Leu Lys Ser Val Gly Val Lys Asp Ser Lys Lys Leu Asp Arg
 25 35 40 45
 26 Arg Lys Arg Glu Glu Leu Tyr Asn Ile Ile Lys Ser Leu Cys Lys
 27 50 55 60
 28 Val Lys Val Leu Lys Ile Ser Val Glu Asp Leu Asn Arg Leu Met
 29 65 70 75
 30 Glu Tyr Met Ser Ile Asn Glu Ile Leu Lys Arg Ala Tyr Val Glu
 31 80 85 90
 32 Ile Ile Arg Ser Leu Met Pro Lys Val Val Tyr Ile Asp Cys Pro
 33 95 100 105
 34 Asp Ile Asn Val Glu Arg Phe Lys His Glu Ile Glu Glu Arg Thr
 35 110 115 120
 36 Gly Val Glu Val Phe Ala Ser His Lys Ala Asp Glu Ile Tyr Pro
 37 125 130 135
 38 Ile Val Ser Ile Ala Ser Ile Val Ala Lys Val Glu Arg Asp Phe
 39 140 145 150
 40 Glu Ile Asp Lys Leu Lys Lys Ile Tyr Gly Asp Phe Gly Ser Gly
 41 155 160 165
 42 Tyr Pro Ser Asp Leu Arg Thr Ile Glu Phe Leu Arg Ser Tyr Leu
 43 170 175 180
 44 Arg Glu His Lys Ser Phe Pro Pro Ile Val Arg Lys Arg Trp Lys
 45 185 190 195

see pg 1-4, 6

**Does Not Comply
 Corrected Diskette Needed**

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/526,073

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Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\07062006\J526073.raw

46 Thr Leu Lys Arg Leu Thr Thr His Thr Leu Ser Asp Phe Phe Glu
47 200 205 210

48 Val

49 211

152 <210> SEQ ID NO: 10

153 <211> LENGTH: 560

154 <212> TYPE: DNA

155 <213> ORGANISM: Hepatitis B virus

157 <400> SEQUENCE: 10

```
158 ccttcccatg gctgctcggg tgtgctgccg actggatcct gcgcgggacg tcctttgtct 60
159 acgtcccgtc ggcgctgaat cccgcggacg acccgtctcg gggccgtttg ggcctctacc 120
160 gtcccttget ttctctgccg ttccagccga ccacggggcg cacctctctt tacgcggtct 180
161 ccccgctctg gcccttctcat ctgccggacc gtgtgcactt cgcttcacct ctgcacgtcg 240
162 catggagacc accgtgaacg gccaccaggt cttgcccagg ctcttacata agaggactct 300
163 tggactctca gcaatgtcaa caaccgacct tgaggcatac ttcaaagact gtttgtttaa 360
164 agactgggag gagttggggg aggagattag gttaaaggct tttgtactag gaggctgtag 420
165 gcataaattg gtctgttcac cagcaccatg caactttttc acctctgcct aatcatctca 480
166 tgttcatgtc ctactgttca agcctccaag ctgtgccttg ggtggccttg gggcatggac 540
```

B--> 167 attgaccctg ataaagaatt

560 ← insert

see p. 6

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/526,073

DATE: 07/06/2006
TIME: 13:47:50

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\07062006\J526073.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 75
Seq#:4; Line(s) 87
Seq#:11; Line(s) 175
Seq#:12; Line(s) 188

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/526,073

DATE: 07/06/2006
TIME: 13:47:50

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\07062006\J526073.raw

even explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 18

Seq#:4; N Pos. 18

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/526,073

DATE: 07/06/2006

TIME: 13:47:50

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\07062006\J526073.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:9
L:79 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
L:79 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:91 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
L:91 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:560 SEQ:10

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer RN-F1 for cloning a gene encoding a polypeptide having a RNaseH activity from Archaeoglobus profundus

<400> 3

ggcattgatg aggctggnar rgg

23

see p. 4 for error explanation

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer RN-R2 for cloning a gene encoding a polypeptide having a RNaseH activity from Archaeoglobus profundus

<400> 4

ggtagggaaa gctgraanng

20

see p. 4